48. **(New)** The method of claim 46, wherein said binding of the allelic variant is detected by use of an assay for HGT-1 activity.

REMARKS

Claims 1-31 were pending in the application. Claims 1-22, and 25-31 have been canceled without prejudice, as being drawn to a non-elected invention. Claims 23 and 24 have also been cancelled and new claims 32-48 have been added. Accordingly, after the amendments presented herein have been entered, claims 32-48 will remain pending. Applicants respectfully submit that claims 32-48 are directed towards the elected invention. For the Examiner's convenience all of the pending claims are set forth in Appendix A.

Support for the new claims can be found throughout the specification and in the claims as originally filed. Specifically, support for claims 32 and 33 can be found at, for example, page 51, lines 23-27 of the specification. Support for claims 34, 43 and 47 can be found at, for example, page 52, line 18 through page 55 line 7 of the specification. Support for claims 35 and 44 can be found at, for example, page 35, lines 3-10 of the specification. Support for claim 36 can be found at, for example, page 54, lines 17-26 of the specification. Support for claims 37, 41 and 48 can be found at, for example, page 50, lines 29-35 of the specification. Support for claims 38 and 39 can be found at, for example, page 52, lines 18-21 of the specification. Support for claims 40 and 45 can be found in, for example, claim 24 as originally filed. Support for claims 42, and 46 can be found at, for example, page 3, line 3 through page 4, line 2 of the specification.

No new matter has been added. Any cancellation of the claims should in no way be construed as an acquiescence to any of the Examiner's rejections and was done solely to expedite the prosecution of the application. Applicants reserve the right to pursue the claims as originally filed in this or a separate application(s).

CONCLUSION

In view of the amendments and remarks set forth above, it is respectfully submitted that this application is in condition for allowance. If there are any remaining issues or the Examiner believes that a telephone conversation with Applicants' Attorney would be helpful in expediting prosecution of this application, the Examiner is invited to call the undersigned at (617) 227-7400.

Respectfully submitted,

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Appendix A

32. A method for identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:2, the method comprising:

a) contacting a cell expressing the polypeptide with a test compound under conditions suitable for binding to the polypeptide; and

b) determining whether the polypeptide binds to the test compound.

33. A method for identifying a compound which binds to a polypeptide consisting of the amino acid sequence of SEQ ID NO:2, the method comprising:

a) contacting a cell expressing the polypeptide with a test compound under conditions suitable for binding to the polypeptide; and

b) determining whether the polypeptide binds to the test compound.

34. The method of claim 23 or 24, wherein said binding of the polypeptide is detected by direct binding of the test compound to the polypeptide.

35. The method of claim 34, wherein said direct binding is determined by lysing the cell and performing an immunoprecipitation.

36. The method of claim 34, wherein said direct binding is determined by a yeast two-hybrid assay.

37. The method of claim 32, wherein said binding of the polypeptide is detected by use of an assay for HGT-1activity.

38. A method for identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:2, the method comprising:

a) contacting the polypeptide with a test compound under conditions suitable for binding to the polypeptide; and

b) determining whether the polypeptide binds to the test compound.

39. A method for identifying a compound which binds to a polypeptide consisting of the amino acid sequence of SEQ ID NO:2, the method comprising:

a) contacting the polypeptide with a test compound under conditions suitable for binding to the polypeptide; and

b) determining whether the polypeptide binds to the test compound.

40. The method of claim 38 or 39, wherein said binding of the polypeptide is detected by the use of a competition binding assay.

41. The method of claim 38 or 39, wherein said binding of the polypeptide is detected by use of an assay for HGT-1 activity.

42. A method for identifying a compound which binds to a polypeptide comprising at least 10 contiguous amino acids of SEQ ID NO:2, the method comprising:

a) contacting the polypeptide with a test compound under conditions suitable for for binding of the polypeptide; and

b) determining whether the polypeptide binds to the test compound.

43. The method of claim 42, wherein said binding of the polypeptide is detected by direct binding of the test compound to the polypeptide.

44. The method of claim 43, wherein said direct binding is determined by an immunoprecipitation.

45. The method of claim 42, wherein said binding of the polypeptide is detected by the use of a competition binding assay.

46. A method for identifying a compound which binds to a naturally occurring allelic variant of a polypeptide consisting of the amino acid sequence of SEQ ID NO:2, wherein the allelic variant is encoded by a nucleic acid molecule which hybridizes under

stringent conditions to the complement of a nucleic acid molecule consisting of SEQ ID NO:1 or 3, the method comprising:

a) contacting a cell expressing the allelic variant with a test compound under conditions suitable for binding of the allelic variant; and

b) determining whether the allelic variant binds to the test compound.

47. The method of claim 46, wherein said binding of the allelic variant is detected by direct binding of the test compound to the allelic variant.

48. The method of claim 46, wherein said binding of the allelic variant is detected by use of an assay for HGT-1 activity.